

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: September 1, 2002, 05:37:35 ; Search time 5265 Seconds
(without alignments)
16995.607 Million cell updates/sec

Title: US-09-730-559B-1

Perfect score: 4276
Sequence: 1 ttctaccgcttttccctgc.....atcagaataaaaaaaaaa 4276

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

Database :

GenEmbl:*
1: gb_ba:*
2: gb_hlg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_ph:*
7: gb_pl:*
8: gb_pr:*
9: gb_ro:*
10: gb_ro:*
11: gb_ro:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vl:*
30: em_hlg_hum:*
31: em_hlg_inv:*
32: em_hlg_other:*
33: em_hlgo_inv:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Match Length	DB ID	Description
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1	3690.4	86.3	167659	2	AC023404	AC023404 Homo sapi
2	3690.4	86.3	175793	2	AC083300	AC083300 Homo sapi
3	3690.4	86.3	160130	2	AC093275	AC093275 Homo sapi
4	2480.4	56.0	157340	2	AC027609	AC027609 Homo sapi
5	912.6	21.3	6380	9	AB051460	AB051460 Homo sapi
6	467.4	10.9	212601	2	AL662793	AL662793 Mus muscu
7	467.4	10.9	249657	2	AL669946	AL669946 Mus muscu
8	430	10.1	5715	9	AB023157	AB023157 Homo sapi
9	364.6	9.3	71171	2	AC100917	AC100917 Mus muscu
10	304.6	7.1	3114	3	AY052043	AY052043 Drosophi
11	304.6	7.1	103054	2	AC014803	AC014803 Drosophi
12	304.6	7.1	181720	3	AC010114	AC010114 Drosophi
13	304.6	7.1	287018	3	AE003553	AE003553 Drosophi
14	240.6	5.6	205307	2	AC009968	AC009968 Homo sapi
15	238	5.6	97037	9	AP000474	AP000474 Homo sapi
16	238	5.6	126000	9	AP000744	AP000744 Homo sapi
17	238	5.6	135038	2	HEMRYXD703	HEMRYXD703 Homo sapi
18	238	5.6	180112	2	AF002354	AF002354 Homo sapi
19	237	5.6	113687	2	AC069281	AC069281 Homo sapi
20	233.8	5.3	179245	2	AC069281	AC069281 Homo sapi
21	231.4	5.4	203959	2	AC064827	AC064827 Homo sapi
22	230.4	5.4	133475	2	AC006254	AC006254 Homo sapi
23	230.2	5.4	183000	2	AC091489	AC091489 Homo sapi
24	230.2	5.4	181532	2	CNS01DM2	AL1136298 Human chr
25	230.2	5.4	187696	2	AC008785	AC008785 Homo sapi
26	229.4	5.4	155691	2	AC016868	AC016868 Homo sapi
27	229.4	5.4	214872	2	AC009720	AC009720 Homo sapi
28	228.6	5.3	166889	2	AC027008	AC027008 Homo sapi
29	228.6	5.3	167412	2	AL356352	AL356352 Homo sapi
30	228.6	5.3	159663	2	AL158307	AL158307 Homo sapi
31	228.6	5.3	241288	2	AC011499	AC011499 Homo sapi
32	228.4	5.3	147224	2	AP003779	AP003779 Homo sapi
33	228.4	5.3	151252	2	AC087464	AC087464 Homo sapi
34	228.4	5.3	157998	9	AL353562	AL353562 Homo sapi
35	228.4	5.3	112425	2	AC092573	AC092573 Homo sapi
36	228.4	5.3	208729	2	AC012052	AC012052 Homo sapi
37	228.4	5.3	215177	2	AC011667	AC011667 Homo sapi
38	228.4	5.3	162589	2	AC012052	AC012052 Homo sapi
39	228	5.3	180465	9	AC074011	AC074011 Homo sapi
40	228	5.3	196769	2	AC092164	AC092164 Homo sapi
41	228	5.3	207922	2	AC093164	AC093164 Homo sapi
42	227.8	5.3	84388	9	AL589984	AL589984 Human DNA
43	227.4	5.3	159634	2	AC010193	AC010193 Homo sapi
44	227.2	5.3	163891	9	AC092647	AC092647 Homo sapi
45	227	5.3	172789	2	AC104020	AC104020 Homo sapi

ALIGNMENTS

RESULT 1	AC023404	167659 bp	DNA	linear	HTG 01-MAR-2000
LOCUS	AC023404				
DEFINITION	Homo sapiens clone RP11-619L12, WORKING DRAFT SEQUENCE, 10				
ACCESSION	AC023404				
VERSION	AC023404.2	GI:7139760			
KEYWORDS	HTG; HTGS_PHASE1; HTGS_DRAFT.				
SOURCE	human.				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.				
TITLE	1 (bases 1 to 167659)				
JOURNAL	Homo sapiens, clone RP11-619L12				
REFERENCE	Unpublished				
AUTHORS	Bliren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barne, N., Bede, F., Boguslavsky, L., Boukhalter, B., Brown, A., Burkett, G., Campoliano, A., Castle, A., Chepel, Y., Colangelo, M., Collins, S., Colliore, A., Cooke, P., Dearellano, K., Dewar, K., Dodge, S., Domino, M., Doyle, M., Fenestor, J., Ferreira, P., FitzHugh, W., Forrest, C., Gage, D.,				

Query Match	Similarity	86.3%	Score 3690.4	DB 2:	Length 167659
Best Local	Similarity	99.64%	Pred. No. 0:		
Matches 3732;	Conservative	0;	Mismatches	11;	Indels 5; Gaps 3
QY 530	gtgagagcttggaatggtcaatgatgacggtcctacatcggaagctgtgtctcaagctgtggaatgat	589			
Db 133956	gttgagacttgcgcattatataatgatatcggctctatcttgagaggtgtgtctctacgttggaattgat	134015			
QY 590	accggaaccttgagcttaataatacccaaaaggagcttgggaagttgctgtctctcaatacaaacg	649			
Db 134016	accggaaccttgcagctcttataataccctaaaggagcttggaagctgtgctgtctcttataatcag	134075			
QY 650	agctacatagctgcgtcatcgaatgctccgcttctgttcagccgcgcagctggagagataatacaaa	709			
Db 134076	agtttaataatgcctgcctatatacagcccttctgttcagctgcgcagctatgagagatataatataa	134135			
QY 710	cgggtgaagctctatactacatcttttggaaaattctagaatgtgctctctaaipgttgatt	769			
Db 134136	cgggtgaagctctatactacatcttttggaaaattctagaatgtgctctctctaaatgttgatt	134195			
QY 770	accaataataagaaaggagagcatcttatalgcaataaagtgaagcttgacaattttgacctat	829			
Db 134196	accgaataattgaaacggagagcattttatgcaataaaggagagctgacacattttgacctat	134255			
QY 830	agagatcaatcatgctcatalaatacagaataatgctccatgaattccttccatccctca	889			
Db 134256	agagatcaatcatgctcatalaatacagaataatgctccatgaattccttccatccctca	134315			
QY 890	gtcttttgtagagccatactcagaacacatactcaactcaactgagttaaattatctctctca	949			
Db 134316	gttttttgtagagccatactcagaacacatactcaactcaactgagttaaattatctctctca	134375			
QY 950	acttcattcaatcctacatccatccgtctcatctcatctatctactagttttgtaagcatccaat	1009			
Db 134376	acttcattcaatcctacatccatccgtctcatctcatctatctactagttttgtaagcatccaat	134435			
QY 1010	aaataatctcgaatcactctgtctcgtgttataataagataaagaaagaagatccgcttg	1069			
Db 134436	aaataatctcgaatcactctgtctcgtgttataataagataaagaaagaagatccgcttg	134495			
QY 1070	aggtctctgcacctcttcttctgtctgttttaactcctgggaataaggagaagccctcagc	1129			
Db 134496	aggtttctcgcacctcttcttctgtctgttttttaactcctgggaataaggagaagccctcagc	134555			

[illegible]

QY	2210	atcaagacgtgaattctgtctccctcgcaatgaatacctctggccagctctcaatccac	2269
D	135633	ATTGAGACTGAATTGTGTCTCTCGCAATTAATCCTTGGCCAGATGTCATGTCATC	135692
QY	2270	tgtgaacattatggaaacagccctagaagccaaagaacccagctgctccctatgacctgtcc	2329
D	135693	TGTAGACATTATGAGACACACCCCTAGAGGCGCAAGACCAGTGCCTCTATTGCGCTCT	135752
QY	2330	tcctcgagcttcgtgaacactctctctccctctgttactttatcttttttagttaaaac	2389
D	135753	TCCGGGCTTCGGAGACCT	135812
QY	2390	tctttttagagggaggggtctcaactctgtccaccaagcctggagacagaatacacaatcag	2449
D	135813	TTTTTTTTAGAGGAGAGGCTCTCACTCTGTCAACCCAGCGCTGAGACAGAAATCAATCATG	135872
QY	2450	actcaacgtcgtctctctctctctcttctgttcatggtcaatctctgtgctcagatctccgtcag	2509
D	135873	ACTCACTGCAATGTCTCTCCCTTGTGTTGTTCAATGCGCTAATCTGCTCAGATTCCTGTACAG	135932
QY	2510	agctcggttgcacacagtgctgtgtgacagccctgcctgaagaaggatttcaacccatgaatctc	2569
D	135933	AGCTGGGTGGCACACATGCTGTGTGACACCCGCTGTAAGGAGATTCAACCATGAATCTC	135992
QY	2570	tccagacataaataaacacagctctctttcttagctgtagaataataaacaggtgtacgttta	2629
D	135993	TCCAGACTTAATAATTAACACAGCTCTTTCTTACTCTATATTAATTAACACAGGTGATGTGTA	136053
QY	2610	atgctgtgaaaggttccatgacatgacaggttggccgatalagaaagcctgaaacagccagattta	2689
D	136053	ATGCTTTAAAGGTTCACATGACAGAGTTGGCGGATGAGAACCTGTGAACAGGCCCATTTTGA	136112
QY	2690	gaactcaacctcgtacattttaaagcctcagtgaaacattcttcaactgtagaaagaacaagca	2749
D	136113	GAAATTCACCTCTGACTTTTAACTTAACGTCAAGCTTAACCATTTCTACTGTGAAGAAACAAGCA	136172
QY	2750	gggttttagagctgtgaatccctatgctgcacac - ttttttttttttaaagaggttccag	2808
D	136173	GGGTTTAAAGCTGTGAATCCATTCAGCTGCTGCACATCTTTTTTTAAACAGAGTCCAG	136232
QY	2809	gtttgtgattataaacccaacatggtgtacacataataagaaacccagccagagctttc	2868
D	136233	GTTGTGATTATTAACCAACAATGTTGTACACTATTAATTAAGAAACACAGACCGGCTTTT	136292
QY	2869	acgacagctcagatctctgtgacgagtagtcagacatcttccacacgacattgaaatctg	2928
D	136293	ACGACACCTCAGATCTTCTGTGACGACAGTAGTCAAGCATCTTCACACCACTTGAAATATG	136352
QY	2929	aagtcgagttgtgtgaaccttgatgacatcctaatgtatgtatttgttttaaatatgattccac	2988
D	136353	AAGTCGAGTTGTGTGAACCTTGGAATCATCTATGTATGATTTTGTTTAAATTAATGATTCAC	136412
QY	2989	atagagacaaaaatccagatccacacataataaagaagaaggtttatgtctatgaaataatcc	3048
D	136413	ATATGACAAAAATCCAGATCCACTTAATTAAATAGAGGTTTATGCTATGAAATATCTCC	136472
QY	3049	tgtgtgtttaatctcataacatctcagctctaaacagcttggtctcaactcaatgattgtcgc	3108
D	136473	TGTGTGTTAAATCTCAATCAATTCAGACTTAACAGTGTGGCTTCATCTCAGATGCTCC	136532
QY	3109	tcaaatcttttccctttaaagagatgattatctaataaagaaaaaaatgtaaaatgtag	3168
D	136533	TCAAAATCCTTTTCCCTTAAAGAGATGTTATTATTAACG - AAAAAAAGTTAAATGATAG	136593
QY	3169	ataataaagaacccctactaggttctttaaagaatgaacataccatcttcaagtaaatgata	3228
D	136592	ATATATAAAGCCCTTACTAGTGTCTTAAAGATGAACATTCATCTATTTTCAAGTAATGATA	136653
QY	3229	attagtcctctctctcttgggacaccttggaaacagatcattccagatagtggtgtgaaatgc	3288
D	136652	ATTAGTCTCTCTCTTGTGGGCACTCTGGAACAGATTCTATTCAGATAGTGGGTGGAATATG	136711
QY	3289	acatgtagtgaagcatctgtgctgacctagtcacgtgaataatgtaaaccttatttctgatt	3348

Db	136712	ACATGATATGTAAAGCATTTGCGGCTAGTCACCTAAATAAGTAACTCTATTATTGATT	136771
Db 136712	ACATGATATGTAAAGCATTTGCGGCTAGTCACCTAAATAAGTAACTCTATTATTGATT		136771
Qy 3349	gcagagtcggaagcttaagccatactctcttgagatcaagctgtgagaaatgcgaagggc		3408
Db 136772	GCAGGTCGAAGTTAAGCCATATGCTTGAGATGATACACTGTGATGAATGTACAGGGGC		136831
Qy 3409	cggcttctggggggaattctgcacattctctgscgaatgtaactgtctctcaglatla		3468
Db 136832	CGCTTCTGGGGGAATTTGCTCCATTCTTCTGTGCGCAAGTTACTGTCTCAGTATTA		136891
Qy 3469	cctgtgaatctctcctggctctcatccattcctcgtctcgtgcaggaaattccaaagccct		3528
Db 136892	CTGTGAATTTCTCGCGCTGCTATTCATTCTCGCTCGAGGGAATTCACAAAGCCCT		136951
Qy 3529	ggttgaaaggaagcggatgacgcgcctcggcabaattccattccgcttgaaactaaaggatac		3588
Db 136952	GGTGAAGGAAGCGGTGACCGCCCTCGGCATATTTCTTCCTGGACATTAAGATTAAC		137011
Qy 3589	tgcagtcgctcattcttcagggcctcagaataatgtgacacctctctcatctcagcccttc		3648
Db 137012	TGCAGTGCCTATTTCAGGCCCTCAGAAATAGTCACTCTGTCTATTCTACCCCTTC		137071
Qy 3649	ctcaacctctcagctctgacatgctcctcttgtaacagctcgtgaacttaactagatata		3708
Db 137072	CTCACTCTCTCCGCTGGCATGTCTTTGTATCACTGTAACTTACTTAAGATTA		137131
Qy 3709	tggaaaaaatgacctataataatagttgtttgtatgattctgtgtacatggaacaaatc		3768
Db 137132	TGAAAAAATGACCTTAATATATAGTGTGTTGTATGATCTGTGTCTACGTCAACAAATAT		137191
Qy 3769	gaactcctcttcctgatactgcatcggtgtgtgataagaaagtttattctctgtttgctcg		3828
Db 137192	GAACCTCTTTTCGTATTCCTACCTCGGGGTGATGGAAGTTATCTCTGTGTTCTGG		137251
Qy 3829	aaacccaagagatccaaactctcgcacaacttctcttagagagagagaagaatatlaa		3888
Db 137252	AAACCAAGAGATCCAAACTCTCTGCAACATTTCTTAAAGAGAGAGAAATATTATA		137311
Qy 3889	agagaaatgaaacaatagatcattcttggtttttaaataattcgttaataataaac		3948
Db 137312	AGAGAAATGAACAATAAGATATTTGGGTTTAAATTAATTAATTAATTAATTAATTAAC		137371
Qy 3949	ataaagaatcacttattataaataacatgacaatgacaatatacactatcgtctatgaca		4008
Db 137372	ATAATGAATACCTTTATTAATAATTAACATCAACAATAACACTATGGCTTATCGACA		137431
Qy 4009	gttttcccccaaggaagtgctcttgacctcttcctctcttcttcttcttcttctcacttc		4068
Db 137432	GTTTTTCCCCAGGAAGTGCTTTGGCTTTCTCTCTTTTCTTTTCTTTTCTTTTCTCTT		137491
Qy 4069	tttgctctctctcttcttctcactctctttaaattttttaaagcaatgaggaagtta		4128
Db 137492	TTTGCTCTCTCTCTTTTTCATCCCTTTTAATTTTAAAGCAATGAGGAAGTTA		137551
Qy 4129	acaaattttatgaaagagcaatgtaagaacaaatgataagaagaacgtgagcaac		4188
Db 137552	ACAAATTTTAATGAAAGACATGTAAGCAACAAATGCAATACCAAAACGTGACACAC		137611
Qy 4189	ataataatcaattcagaaggtctgagagcgaacataattctcatctacccctaaagtt		4248
Db 137612	ATAATTAATTAATTTGAGGTTTGAAGGTACATTAATTTTCATTATTCCTCAAAAAGTT		137671
Qy 4249	acacacacatcagaataaataaataaataa 4276		
Db 137672	ACACACACATCAGAAAAAATTAATAAAAAA 137699		

RESULT 2

AC093300/c

LOCUS

DEFINITION

AC093300

175793 bp

DNA

linear

HTG 16-AUG-2001

Homo sapiens chromosome 5 clone RP11-560A7, WORKING DRAFT SEQUENCE.

19 unordered pieces.

Db 78523 TTTTATTAAGAGGAGGCTCTGACCTGTCACCCAGGCTGAGACACAGATCATCATG 78564
 QY 2450 ACTGAGGAGGAGGCTCTGACCTGTCACCCAGGCTGAGACACAGATCATCATG 2509
 Db 78563 ACTGAGGAGGAGGCTCTGACCTGTCACCCAGGCTGAGACACAGATCATCATG 78504
 QY 2510 AGGTGAGGAGGAGGCTCTGACCTGTCACCCAGGCTGAGACACAGATCATCATG 2569
 Db 78503 AGGTGAGGAGGAGGCTCTGACCTGTCACCCAGGCTGAGACACAGATCATCATG 78444
 QY 2570 TCCAGGAGGAGGCTCTGACCTGTCACCCAGGCTGAGACACAGATCATCATG 2629
 Db 78443 TCCAGGAGGAGGCTCTGACCTGTCACCCAGGCTGAGACACAGATCATCATG 78384
 QY 2630 ATGCTGAGGAGGAGGCTCTGACCTGTCACCCAGGCTGAGACACAGATCATCATG 2689
 Db 78383 ATGCTGAGGAGGAGGCTCTGACCTGTCACCCAGGCTGAGACACAGATCATCATG 78324
 QY 2690 GAAATTCAGGAGGAGGCTCTGACCTGTCACCCAGGCTGAGACACAGATCATCATG 2749
 Db 78323 GAAATTCAGGAGGAGGCTCTGACCTGTCACCCAGGCTGAGACACAGATCATCATG 78264
 QY 2750 GGGGTTTGAAGGAGGAGGCTCTGACCTGTCACCCAGGCTGAGACACAGATCATCATG 2808
 Db 78263 GGGGTTTGAAGGAGGAGGCTCTGACCTGTCACCCAGGCTGAGACACAGATCATCATG 78204
 QY 2809 GTTGTGATTAAGGAGGAGGCTCTGACCTGTCACCCAGGCTGAGACACAGATCATCATG 2868
 Db 78203 GTTGTGATTAAGGAGGAGGCTCTGACCTGTCACCCAGGCTGAGACACAGATCATCATG 78144
 QY 2869 AAGGAGGAGGAGGAGGCTCTGACCTGTCACCCAGGCTGAGACACAGATCATCATG 2928
 Db 78143 AAGGAGGAGGAGGAGGCTCTGACCTGTCACCCAGGCTGAGACACAGATCATCATG 78084
 QY 2929 AAGGAGGAGGAGGAGGCTCTGACCTGTCACCCAGGCTGAGACACAGATCATCATG 2988
 Db 78083 AAGGAGGAGGAGGAGGCTCTGACCTGTCACCCAGGCTGAGACACAGATCATCATG 78024
 QY 2989 AATGAGGAGGAGGAGGCTCTGACCTGTCACCCAGGCTGAGACACAGATCATCATG 3048
 Db 78023 AATGAGGAGGAGGAGGCTCTGACCTGTCACCCAGGCTGAGACACAGATCATCATG 77964
 QY 3049 TGGGAGGAGGAGGAGGCTCTGACCTGTCACCCAGGCTGAGACACAGATCATCATG 3108
 Db 77963 TGGGAGGAGGAGGAGGCTCTGACCTGTCACCCAGGCTGAGACACAGATCATCATG 77904
 QY 3109 TCAATTCAGGAGGAGGAGGCTCTGACCTGTCACCCAGGCTGAGACACAGATCATCATG 3168
 Db 77903 TCAATTCAGGAGGAGGAGGCTCTGACCTGTCACCCAGGCTGAGACACAGATCATCATG 77845
 QY 3169 AATAAAGGAGGAGGAGGCTCTGACCTGTCACCCAGGCTGAGACACAGATCATCATG 3228
 Db 77844 AATAAAGGAGGAGGAGGCTCTGACCTGTCACCCAGGCTGAGACACAGATCATCATG 77785
 QY 3229 ATTGAGGAGGAGGAGGCTCTGACCTGTCACCCAGGCTGAGACACAGATCATCATG 3288
 Db 77784 ATTGAGGAGGAGGAGGCTCTGACCTGTCACCCAGGCTGAGACACAGATCATCATG 77725
 QY 3289 AAGTGAAGGAGGAGGAGGCTCTGACCTGTCACCCAGGCTGAGACACAGATCATCATG 3348
 Db 77724 AAGTGAAGGAGGAGGAGGCTCTGACCTGTCACCCAGGCTGAGACACAGATCATCATG 77665
 QY 3349 GAGGAGGAGGAGGAGGCTCTGACCTGTCACCCAGGCTGAGACACAGATCATCATG 3408
 Db 77664 GAGGAGGAGGAGGAGGCTCTGACCTGTCACCCAGGCTGAGACACAGATCATCATG 77605
 QY 3409 CGGTGAGGAGGAGGAGGCTCTGACCTGTCACCCAGGCTGAGACACAGATCATCATG 3468
 Db 77604 CGGTGAGGAGGAGGAGGCTCTGACCTGTCACCCAGGCTGAGACACAGATCATCATG 77545
 QY 3469 CTGTGAAGGAGGAGGAGGCTCTGACCTGTCACCCAGGCTGAGACACAGATCATCATG 3528
 Db 77544 CTGTGAAGGAGGAGGAGGCTCTGACCTGTCACCCAGGCTGAGACACAGATCATCATG 77485

QY 3529 GGTGAAGGAGGAGGAGGCTCTGACCTGTCACCCAGGCTGAGACACAGATCATCATG 3588
 Db 77484 GGTGAAGGAGGAGGAGGCTCTGACCTGTCACCCAGGCTGAGACACAGATCATCATG 77425
 QY 3589 TGGGAGGAGGAGGAGGCTCTGACCTGTCACCCAGGCTGAGACACAGATCATCATG 3648
 Db 77424 TGGGAGGAGGAGGAGGCTCTGACCTGTCACCCAGGCTGAGACACAGATCATCATG 77365
 QY 3649 CTAAGGAGGAGGAGGAGGCTCTGACCTGTCACCCAGGCTGAGACACAGATCATCATG 3708
 Db 77364 CTAAGGAGGAGGAGGAGGCTCTGACCTGTCACCCAGGCTGAGACACAGATCATCATG 77305
 QY 3709 TGAAGGAGGAGGAGGAGGCTCTGACCTGTCACCCAGGCTGAGACACAGATCATCATG 3768
 Db 77304 TGAAGGAGGAGGAGGAGGCTCTGACCTGTCACCCAGGCTGAGACACAGATCATCATG 77245
 QY 3769 GAGGAGGAGGAGGAGGCTCTGACCTGTCACCCAGGCTGAGACACAGATCATCATG 3828
 Db 77244 GAGGAGGAGGAGGAGGCTCTGACCTGTCACCCAGGCTGAGACACAGATCATCATG 77185
 QY 3829 AAGGAGGAGGAGGAGGCTCTGACCTGTCACCCAGGCTGAGACACAGATCATCATG 3888
 Db 77184 AAGGAGGAGGAGGAGGCTCTGACCTGTCACCCAGGCTGAGACACAGATCATCATG 77125
 QY 3889 GAGGAGGAGGAGGAGGCTCTGACCTGTCACCCAGGCTGAGACACAGATCATCATG 3948
 Db 77124 GAGGAGGAGGAGGAGGCTCTGACCTGTCACCCAGGCTGAGACACAGATCATCATG 77065
 QY 3949 AATAAGGAGGAGGAGGCTCTGACCTGTCACCCAGGCTGAGACACAGATCATCATG 4008
 Db 77064 AATAAGGAGGAGGAGGCTCTGACCTGTCACCCAGGCTGAGACACAGATCATCATG 77005
 QY 4009 GTTGTGAGGAGGAGGAGGCTCTGACCTGTCACCCAGGCTGAGACACAGATCATCATG 4068
 Db 77004 GTTGTGAGGAGGAGGAGGCTCTGACCTGTCACCCAGGCTGAGACACAGATCATCATG 76945
 QY 4069 TGGGAGGAGGAGGAGGCTCTGACCTGTCACCCAGGCTGAGACACAGATCATCATG 4128
 Db 76944 TGGGAGGAGGAGGAGGCTCTGACCTGTCACCCAGGCTGAGACACAGATCATCATG 76885
 QY 4129 AAGTGAAGGAGGAGGAGGCTCTGACCTGTCACCCAGGCTGAGACACAGATCATCATG 4188
 Db 76884 AAGTGAAGGAGGAGGAGGCTCTGACCTGTCACCCAGGCTGAGACACAGATCATCATG 76825
 QY 4189 ATTGAAGGAGGAGGAGGCTCTGACCTGTCACCCAGGCTGAGACACAGATCATCATG 4248
 Db 76824 ATTGAAGGAGGAGGAGGCTCTGACCTGTCACCCAGGCTGAGACACAGATCATCATG 76765
 QY 4249 ACCGAGGAGGAGGAGGCTCTGACCTGTCACCCAGGCTGAGACACAGATCATCATG 4276
 Db 76764 ACCGAGGAGGAGGAGGCTCTGACCTGTCACCCAGGCTGAGACACAGATCATCATG 76737

RESULT 3
 AC093275 180130 bp DNA linear HTG 16-AUG-2001
 LOCUS AC093275
 DEFINITION Homo sapiens chromosome 5 clone RP11-379A13, WORKING DRAFT
 AC093275
 VERSION AC093275.1 GI:15193409
 KEYWORDS HTG; HTGS; PHASE1; HTGS_DRAFT; HTGS_ACTIVEIN.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 180130)
 AUTHORS DOE Joint Genome Institute.
 TITLE Sequencing of Human Chromosome 5
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 180130)
 AUTHORS DOE Joint Genome Institute.
 TITLE Direct Submission

QY	2589	acacgacaaataatccagatccacctaataaagaggtttagtctatgaataatctcc	3048
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Db 19362 ACCACCAATGAGAAAAAATAAAAA 19389

RESULT 4
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LOCUS AC027609
DEFINITION Homo sapiens chromosome 5 clone RP11-80E21, WORKING DRAFT SEQUENCE,
ACCESSION AC027609
VERSION AC027609.3 GI:9958118
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 157320)
AUTHORS Waterston,R.H.
TITLE The sequence of Homo sapiens clone
JOURNAL Unpublished
2 (bases 1 to 157320)
AUTHORS Waterston,R.H.
TITLE Direct Submission
JOURNAL Submitted (30-MAR-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
COMMENT On Sep 1, 2000 this sequence version replaced gi:7637328.

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----- Genome Center -----
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu/gsc/index.shtml
----- Project Information -----
Center project name: H_NH080E21
----- Summary Statistics -----
Sequencing vector: M13; 100%
Chemistry: Dye-terminator Big Dye; 0% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 14365 bases at least Q40
Consensus quality: 145934 bases at least Q20
Insert size: 16700; agarose-tp
Insert size: 153359; sum-of-contigs
Quality coverage: 3.44 in Q20 bases; agarose-tp
Quality coverage: 3.89 in Q20 bases; sum-of-contigs
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* NOTE: This is a 'working draft' sequence. It currently
* consists of 34 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
*
* 1 1657: contig of 1657 bp in length
* 1658 1737: gap of unknown length
* 1738 3434: contig of 1657 bp in length
* 3435 3535: gap of unknown length
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7278 8325: contig of 1048 bp in length
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8426 8445: contig of 1020 bp in length
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9546 10207: contig of 661 bp in length
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112332 112333: gap of unknown length
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129643 143637: contig of 13993 bp in length
143637 143735: gap of unknown length
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/chromosome="5"
/clone="RP11-80E21"
1..1657
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3535..5136
misc_feature
misc_feature
misc_feature

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Query Match	58.0%	Score 2480.4	DB 2:	Length 157320
Best Local Similarity	99.5%	Pred. No. 0		
Matches 2509	Conservative	0	Mismatches	11
			Indels	2
			Gaps	2

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Db	43666	AAGAAGAAAGTATCGTGTATTCTTAAGACATGGGGAGGCAAGATATGGTATTACA	43600
OY	1816	tgcctccttctgttttttttgaagaatggagtcctctctgcaccagagctgaagtgcagtg	1875
Db	43606	TGCCTCTTGTGTTTGTTTTGAAGATGAGTCTCTCTCGATACCCAGCCTGGAGTGACAGTGG	4354
OY	1876	tacagtccttaagctcaactcccaactctgcgctcccgagttcgaagtatccctgcgcttagc	1935
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Db	42946	TTATGCTGATATCTTGTCACAGATTCCTTTGTACAGCTGAGCTGGGCACACATGCTGTGAC	4288
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